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PCT/DK99/00481

1

SEQUENCE LISTING

<110> M&E Biotech A/S  
HALKIER, Torben  
HAANING, Jesper

<120> Method for Down-Regulating Osteoprotegerin Ligand  
Activity

<130> 22021 PC 1

<140>

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<170> PatentIn Ver. 2.1

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<212> DNA

<213> Homo sapiens

<220>

<221> CDS

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cgcagacaag aaggggaggg agcgggagag ggaggagagc tccgaagcga gagggccgag 180  
cgcc atg cgc cgc gcc agc aga gac tac acc aag tac ctg cgt ggc tcg 229  
Met Arg Arg Ala Ser Arg Asp Tyr Thr Lys Tyr Leu Arg Gly Ser  
1 5 10 15  
gag gag atg ggc ggc ggc ccc gga gcc ccg cac gag ggc ccc ctg cac 277  
Glu Glu Met Gly Gly Gly Pro Gly Ala Pro His Glu Gly Pro Leu His  
20 25 30  
gcc ccg ccg ccg cct gcg ccg cac cag ccc ccc gcc gcc tcc cgc tcc 325  
Ala Pro Pro Pro Pro Ala Pro His Gln Pro Pro Ala Ala Ser Arg Ser  
35 40 45  
atg ttc gtg gcc ctg ctg ggg ctg ggg ctg gcc cag gtt gtc tgc agc 373  
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910

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tca gaa gat ggc act cac tgc att tat aga att ttg aga ctc cat gaa 469  
 Ser Glu Asp Gly Thr His Cys Ile Tyr Arg Ile Leu Arg Leu His Glu  
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aat gca gat ttt caa gac aca act ctg gag agt caa gat aca aaa tta 517  
 Asn Ala Asp Phe Gln Asp Thr Thr Leu Glu Ser Gln Asp Thr Lys Leu  
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 Ile Pro Asp Ser Cys Arg Arg Ile Lys Gln Ala Phe Gln Gly Ala Val  
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 Gln Lys Glu Leu Gln His Ile Val Gly Ser Gln His Ile Arg Ala Glu  
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ctt gaa gct cag cct ttt gct cat ctc act att aat gcc acc gac atc 709  
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cca tct ggt tcc cat aaa gtg agt ctg tcc tct tgg tac cat gat cg 757  
 Pro Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp Arg  
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 Gly Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile  
 195 200 205

gtt aat cag gat ggc ttt tat tac ctg tat gcc aac att tgc ttt cga 853  
 Val Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg  
 210 215 220

cat cat gaa act tca gga gac cta gct aca gag tat ctt caa cta atg 901  
 His His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu Met  
 225 230 235

gtg tac gtc act aaa acc agc atc aaa atc cca agt tct cat acc ctg 949  
 Val Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His Thr Leu  
 240 245 250 255

atg aaa gga gga agc acc aag tat tgg tca ggg aat tct gaa ttc cat 997  
 Met Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe His  
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gaa atc agc atc gag gtc tcc aac ccc tcc tta ctg gat ccg gat cag 1093  
 Glu Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln  
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 Asp Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp Ile Asp  
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&lt;213&gt; Homo sapiens

&lt;400&gt; 2

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Glu Met Gly Gly Gly Pro Gly Ala Pro His Glu Gly Pro Leu His Ala  
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Pro Pro Pro Pro Ala Pro His Gln Pro Pro Ala Ala Ser Arg Ser Met  
 35 40 45

Phe Val Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser Val  
 50 55 60

Ala Leu Phe Phe Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser  
 65 70 75 80

Glu Asp Gly Thr His Cys Ile Tyr Arg Ile Leu Arg Leu His Glu Asn  
 85 90 95

Ala Asp Phe Gln Asp Thr Thr Leu Glu Ser Gln Asp Thr Lys Leu Ile  
 100 105 110

Pro Asp Ser Cys Arg Arg Ile Lys Gln Ala Phe Gln Gly Ala Val Gln  
 115 120 125

Lys Glu Leu Gln His Ile Val Gly Ser Gln His Ile Arg Ala Glu Lys  
 130 135 140

Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala Lys Arg Ser Lys Leu  
 145 150 155 160

Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr Asp Ile Pro  
 165 170 175

Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp Arg Gly  
 180 185 190

Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile Val  
 195 200 205

Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His  
 210 215 220

His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu Met Val  
 225 230 235 240

Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His Thr Leu Met  
 245 250 255

Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe His Phe

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 275 280 285  
 Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp  
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 Glu Met Gly Ser Gly Pro Gly Val Pro His Glu Gly Pro Leu His Pro  
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 Ala Pro Ser Ala Pro Ala Pro Ala Pro Pro Pro Ala Ala Ser Arg Ser  
 35 40 45  
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 Met Phe Leu Ala Leu Leu Gly Leu Gly Gln Val Val Cys Ser  
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 Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile  
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aac gca ggt ttg cag gac tcg act ctg gag agt gaa gac aca cta cct	336
Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro	
100 105 110	
gac tcc tgc agg agg atg aaa caa gcc ttt cag ggg gcc gtg cag aag	384
Asp Ser Cys Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val Gln Lys	
115 120 125	
gaa ctg caa cac att gtg ggg cca cag cgc ttc tca gga gct cca gct	432
Glu Leu Gln His Ile Val Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala	
130 135 140	
atg atg gaa ggc tca tgg ttg gat gtg gcc cag cga ggc aag cct gag	480
Met Met Glu Gly Ser Trp Leu Asp Val Ala Gln Arg Gly Lys Pro Glu	
145 150 155 160	
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Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser	
165 170 175	
ggg tcc cat aaa gtc act ctg tcc tct tgg tac cac gat cga ggc tgg	576
Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp	
180 185 190	
gcc aag atc tct aac atg acg tta agc aac gga aaa cta agg gtt aac	624
Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn	
195 200 205	
caa gat ggc ttc tat tac ctg tac gcc aac att tgc ttt cgg cat cat	672
Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His	
210 215 220	
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Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr	
225 230 235 240	
gtc gtt aaa acc agc atc aaa atc cca agt tct cat aac ctg atg aaa	768
Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys	
245 250 255	
gga ggg agc acg aaa aac tgg tcg ggc aat tct gaa ttc cac ttt tat	816
Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr	
260 265 270	
tcc ata aat gtt ggg gga ttt ttc aag ctc cga gct ggt gaa gaa att	864
Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile	
275 280 285	

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 Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala  
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 35 40 45

Met Phe Leu Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser  
 50 55 60

Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile  
 65 70 75 80

Ser Glu Asp Ser Thr His Cys Phe Tyr Arg Ile Leu Arg Leu His Glu  
 85 90 95

Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro  
 100 105 110

Asp Ser Cys Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val Gln Lys  
 115 120 125

Glu Leu Gln His Ile Val Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala  
 130 135 140

Met Met Glu Gly Ser Trp Leu Asp Val Ala Gln Arg Gly Lys Pro Glu  
 145 150 155 160

Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser  
 165 170 175

Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp  
 180 185 190

Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn  
 195 200 205

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Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His  
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Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr  
 225 230 235 240

Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys  
 245 250 255

Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr  
 260 265 270

Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile  
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 gggagagaac gatcgcgagg cagggcgccc gaactccggg cgccgcgcc atg cgc cgg 178  
 Met Arg Arg  
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gcc agc cga gac tac ggc aag tac ctg cgc agc tcg gag gag atg ggc 226  
 Ala Ser Arg Asp Tyr Gly Lys Tyr Leu Arg Ser Ser Glu Glu Met Gly  
 5 10 15

agc ggc ccc ggc gtc cca cac gag ggt ccg ctg cac ccc gcg cct tct 274  
 Ser Gly Pro Gly Val Pro His Glu Gly Pro Leu His Pro Ala Pro Ser  
 20 25 30 35

gca ccg gct ccg gcg ccg cca ccc gcc gcc tcc cgc tcc atg ttc ctg 322  
 Ala Pro Ala Pro Ala Pro Pro Pro Ala Ala Ser Arg Ser Met Phe Leu  
 40 45 50

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Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser Ile Ala Leu	
55 60 65	
ttc ctg tac ttt cga gcg cag atg gat cct aac aga ata tca gaa gac	418
Phe Leu Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser Glu Asp	
70 75 80	
agc act cac tgc ttt tat aga atc ctg aga ctc cat gaa aac gca ggt	466
Ser Thr His Cys Phe Tyr Arg Ile Leu Arg Leu His Glu Asn Ala Gly	
85 90 95	
ttg cag gac tgc act ctg gag agt gaa gac aca cta cct gac tcc tgc	514
Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro Asp Ser Cys	
100 105 110 115	
agg agg atg aaa caa gcc ttt cag ggg gcc gtg cag aag gaa ctg caa	562
Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln	
120 125 130	
cac att gtg ggg cca cag cgc ttc tca gga gct cca gct atg atg gaa	610
His Ile Val Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala Met Met Glu	
135 140 145	
ggc tca tgg ttg gat gtg gcc cag cga ggc aag cct gag gcc cag cca	658
Gly Ser Trp Leu Asp Val Ala Gln Arg Gly Lys Pro Glu Ala Gln Pro	
150 155 160	
ttt gca cac ctc acc atc aat gct gcc agc atc cca tgc ggt tcc cat	706
Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser Gly Ser His	
165 170 175	
aaa gtc act ctg tcc tct tgg tac cac gat cga ggc tgg gcc aag atc	754
Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp Ala Lys Ile	
180 185 190 195	
tct aac atg acg tta agc aac gga aaa cta agg gtt aac caa gat ggc	802
Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn Gln Asp Gly	
200 205 210	
ttc tat tac ctg tac gcc aac att tgc ttt cgg cat cat gaa aca tgc	850
Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser	
215 220 225	
gga agc gta cct aca gac tat ctt cag ctg atg gtg tat gtc gtt aaa	898
Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr Val Val Lys	
230 235 240	
acc agc atc aaa atc cca agt tct cat aac ctg atg aaa gga ggc agc	946
Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys Gly Gly Ser	
245 250 255	

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acg aaa aac tgg tgg ggc aat tct gaa ttc cac ttt tat tcc ata aat 994  
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 260 265 270 275  
  
 gtt ggg gga ttt ttc aag ctc cga gct ggt gaa gaa att agc att cag 1042  
 Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser Ile Gln  
 280 285 290  
  
 gtg tcc aac cct tcc ctg ctg gat ccg gat caa gat gcg acg tac ttt 1090  
 Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe  
 295 300 305  
  
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 Gly Ala Phe Lys Val Gln Asp Ile Asp  
 310 315  
  
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2299

&lt;210&gt; 6

&lt;211&gt; 316

&lt;212&gt; PRT

&lt;213&gt; Mus musculus

&lt;400&gt; 6

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Ala Pro Ser Ala Pro Ala Pro Ala Pro Pro Pro Ala Ala Ser Arg Ser  
 35 40 45

Met Phe Leu Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser  
 50 55 60

Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile  
 65 70 75 80

Ser Glu Asp Ser Thr His Cys Phe Tyr Arg Ile Leu Arg Leu His Glu  
 85 90 95

Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro  
 100 105 110

Asp Ser Cys Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val Gln Lys  
 115 120 125

Glu Leu Gln His Ile Val Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala  
 130 135 140

Met Met Glu Gly Ser Trp Leu Asp Val Ala Gln Arg Gly Lys Pro Glu  
 145 150 155 160

Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser  
 165 170 175

Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp  
 180 185 190

Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn  
 195 200 205

Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His  
 210 215 220

Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr  
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12

Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys  
 245 250 255

Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr  
 260 265 270

Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile  
 275 280 285

Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala  
 290 295 300

Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp  
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&lt;210&gt; 7

&lt;211&gt; 564

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

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&lt;221&gt; CDS

&lt;222&gt; (1)..(564)

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic PCR  
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 pastoris expression

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&lt;221&gt; misc\_binding

&lt;222&gt; (43)..(84)

&lt;223&gt; His tag

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&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(36)

<223> C-terminal part of *Saccharomyces cerevisiae*  
 alpha-mating factor

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&lt;223&gt; Encoding wild type murine OPGL, residues 158-316

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13

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 His Gln His Gln His Gln His Gln His Gln His Gln Lys Pro Glu Ala  
 20 25 30

cag cca ttc gct cat ctg acc atc aac gct gca tcg atc cct tct ggt 144  
 Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser Gly  
 35 40 45

tct cat aaa gtt acc ctg tct tct tgg tat cac gac cgc ggt tgg gct 192  
 Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp Ala  
 50 55 60

aaa atc tct aac atg acc ctg tct aac ggt aaa ctg aga gtt aac cag 240  
 Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn Gln  
 65 70 75 80

gac ggt ttc tac tac ctg tac gct aac atc tgt ttc aga cat cac gaa 288  
 Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His Glu  
 85 90 95

acc tct ggt tct gtt cca acc gac tac ctg cag ctg atg gtt tac gtt 336  
 Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr Val  
 100 105 110

gtt aaa acc tct atc aaa atc cca tct tca cat aac ctg atg aaa ggt 384  
 Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys Gly  
 115 120 125

ggt tct acc aaa aac tgg tct ggt aac tct gaa ttc cat ttc tac tct 432  
 Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser  
 130 135 140

atc aac gtt ggt ggt ttc ttc aaa ctg aga gct ggt gaa gaa atc tct 480  
 Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser  
 145 150 155 160

atc cag gtt tct aac cct tct ctg ctg gac cca gac cag gac gct acc 528  
 Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr  
 165 170 175

tac ttc ggg gcc ttc aaa gtt cag gac atc gac tag 564  
 Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp  
 180 185

&lt;210&gt; 8

&lt;211&gt; 187

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

<223> Description of Artificial Sequence: Synthetic PCR  
 product with optimum codons for E. coli and P.  
 pastoris expression

0978726260  
 034404

14

&lt;400&gt; 8

Glu Leu Gly Ser Leu Glu Lys Arg Glu Ala Glu Ala His Val Met Lys  
 1 5 10 15  
 His Gln His Gln His Gln His Gln His Gln His Gln Lys Pro Glu Ala  
 20 25 30  
 Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser Gly  
 35 40 45  
 Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp Ala  
 50 55 60  
 Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn Gln  
 65 70 75 80  
 Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His Glu  
 85 90 95  
 Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr Val  
 100 105 110  
 Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys Gly  
 115 120 125  
 Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser  
 130 135 140  
 Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser  
 145 150 155 160  
 Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr  
 165 170 175  
 Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp  
 180 185

&lt;210&gt; 9

&lt;211&gt; 519

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: DNA encoding  
 murine OPGL, residues 158-316, fused to His tag

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(519)

&lt;220&gt;

09787125.031401

&lt;221&gt; misc\_binding

&lt;222&gt; (1)..(42)

&lt;223&gt; His tag

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (43)..(519)

&lt;223&gt; Murine OPGL, residues 158-316

&lt;400&gt; 9

atg	aaa	cac	caa	cac	caa	cat	caa	cat	caa	cat	caa	aaa	cct	48
Met	Lys	His	Gln	His	Gln	His	Gln	His	Gln	His	Gln	Lys	Pro	
1				5				10				15		

gaa	gct	cag	cca	ttc	gct	cat	ctg	acc	atc	aac	gct	gca	tcg	atc	cct	96
Glu	Ala	Gln	Pro	Phe	Ala	His	Leu	Thr	Ile	Asn	Ala	Ala	Ser	Ile	Pro	
			20					25					30			

tct	ggt	tct	cat	aaa	gtt	acc	ctg	tct	tct	tgg	tat	cac	gac	cgc	ggt	144
Ser	Gly	Ser	His	Lys	Val	Thr	Leu	Ser	Ser	Trp	Tyr	His	Asp	Arg	Gly	
			35				40					45				

tgg	gct	aaa	atc	tct	aac	atg	acc	ctg	tct	aac	ggt	aaa	ctg	aga	gtt	192
Trp	Ala	Lys	Ile	Ser	Asn	Met	Thr	Leu	Ser	Asn	Gly	Lys	Leu	Arg	Val	
		50				55					60					

aac	cag	gac	ggt	ttc	tac	tac	ctg	tac	gct	aac	atc	tgt	ttc	aga	cat	240
Asn	Gln	Asp	Gly	Phe	Tyr	Leu	Tyr	Ala	Asn	Ile	Cys	Phe	Arg	His		
65				70					75				80			

cac	gaa	acc	tct	ggt	tct	gtt	cca	acc	gac	tac	ctg	cag	ctg	atg	gtt	288
His	Glu	Thr	Ser	Gly	Ser	Val	Pro	Thr	Asp	Tyr	Leu	Gln	Leu	Met	Val	
				85					90					95		

tac	gtt	gtt	aaa	acc	tct	atc	aaa	atc	cca	tct	tca	cat	aac	ctg	atg	336
Tyr	Val	Val	Lys	Thr	Ser	Ile	Lys	Ile	Pro	Ser	Ser	His	Asn	Leu	Met	
			100					105					110			

aaa	ggt	ggt	tct	acc	aaa	aac	tgg	tct	ggt	aac	tct	gaa	ttc	cat	ttc	384
Lys	Gly	Gly	Ser	Thr	Lys	Asn	Trp	Ser	Gly	Asn	Ser	Glu	Phe	His	Phe	
		115					120					125				

tac	tct	atc	aac	gtt	ggt	ggt	ttc	ttc	aaa	ctg	aga	gct	ggt	gaa	gaa	432
Tyr	Ser	Ile	Asn	Val	Gly	Gly	Phe	Phe	Lys	Leu	Arg	Ala	Gly	Glu	Glu	
		130				135					140					

atc	tct	atc	cag	gtt	tct	aac	cct	tct	ctg	ctg	gac	cca	gac	cag	gac	480
Ile	Ser	Ile	Gln	Val	Ser	Asn	Pro	Ser	Leu	Leu	Asp	Pro	Asp	Gln	Asp	
145					150					155				160		

gct	acc	tac	ttc	ggg	gcc	ttc	aaa	gtt	cag	gac	atc	gac				519
Ala	Thr	Tyr	Phe	Gly	Ala	Phe	Lys	Val	Gln	Asp	Ile	Asp				
				165					170							

T04T00 92F/8760

<210> 10  
 <211> 173  
 <212> PRT  
 <213> Artificial Sequence  
 <223> Description of Artificial Sequence: DNA encoding  
 murine OPGL, residues 158-316, fused to His tag

<400> 10  
 Met Lys His Gln His Gln His Gln His Gln His Gln Lys Pro  
 1 5 10 15  
 Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro  
 20 25 30  
 Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly  
 35 40 45  
 Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val  
 50 55 60  
 Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His  
 65 70 75 80  
 His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val  
 85 90 95  
 Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met  
 100 105 110  
 Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe  
 115 120 125  
 Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu  
 130 135 140  
 Ile Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp  
 145 150 155 160  
 Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp  
 165 170

<210> 11  
 <211> 519  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Fusion of  
 murine OPGL, residues 158-316 with C to S  
 mutation, and His tag

09787126.034401



<220>  
 <221> CDS  
 <222> (1)..(519)

<220>  
 <221> misc\_binding  
 <222> (1)..(42)  
 <223> His tag

<220>  
 <221> misc\_feature  
 <222> (43)..(228)  
 <223> Murine OPGL, residues 158-219

<220>  
 <221> misc\_feature  
 <222> (232)..(519)  
 <223> Murine OPGL, residues 221-316

<220>  
 <221> mutation  
 <222> (229)..(231)  
 <223> tgt (Cys) to tcc (Ser)

<220>

<400> 11  
 atg aaa cac caa cac caa cat caa cat caa cat caa aaa cct 48  
 Met Lys His Gln His Gln His Gln His Gln His Gln Lys Pro  
     1                    5                    10                    15  
 gaa gct cag cca ttc gct cat ctg acc atc aac gct gca tcg atc cct 96  
 Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro  
                     20                    25                    30  
 tct ggt tct cat aaa gtt acc ctg tct tct tgg tat cac gac cgc ggt 144  
 Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly  
                     35                    40                    45  
 tgg gct aaa atc tct aac atg acc ctg tct aac ggt aaa ctg aga gtt 192  
 Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val  
     50                    55                    60  
 aac cag gac ggt ttc tac tac ctg tac gct aac atc tcc ttc aga cat 240  
 Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Ser Phe Arg His  
     65                    70                    75                    80  
 cac gaa acc tct ggt tct gtt cca acc gac tac ctg cag ctg atg gtt 288  
 His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val  
                     85                    90                    95

09787126.031401

18

tac gtt gtt aaa acc tct atc aaa atc cca tct tca cat aac ctg atg 336  
 Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met  
                   100                                  105                                  110

aaa ggt ggt tct acc aaa aac tgg tct ggt aac tct gaa ttc cat ttc 384  
 Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe  
                   115                                  120                                  125

tac tct atc aac gtt ggt ggt ttc ttc aaa ctg aqa gct ggt gaa gaa 432  
 Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu  
                   130                                  135                                  140

atc tct atc cag gtt tct aac cct tct ctg ctg gac cca gac cag gac 480  
 Ile Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp  
                   145                                  150                                  155                                  160

gct acc tac ttc ggg gcc ttc aaa gtt cag gac atc gac 519  
 Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp  
                                   165                                  170

&lt;210&gt; 12

&lt;211&gt; 173

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

<223> Description of Artificial Sequence: Fusion of  
 murine OPGL, residues 158-316 with C to S  
 mutation, and His tag

&lt;400&gt; 12

Met Lys His Gln His Gln His Gln His Gln His Gln His Gln Lys Pro  
           1                                  5                                  10                                  15

Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro  
                   20                                  25                                  30

Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly  
                   35                                  40                                  45

Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val  
           50                                  55                                  60

Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Ser Phe Arg His  
           65                                  70                                  75                                  80

His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val  
                   85                                  90                                  95

Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met  
                   100                                  105                                  110

Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe  
                   115                                  120                                  125

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19

Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu  
 130 135 140

Ile Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp  
 145 150 155 160

Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp  
 165 170

<210> 13  
 <211> 564  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Fusion of  
 murine OPGL, residues 158-316 modified by  
 introduction of tetanus toxoid P30 epitope, and  
 His tag

<220>  
 <221> CDS  
 <222> (1)..(564)

<220>  
 <221> misc\_binding  
 <222> (1)..(42)  
 <223> His tag

<220>  
 <221> misc\_feature  
 <222> (43)..(336)  
 <223> Murine OPGL, residues 158-255

<220>  
 <221> misc\_feature  
 <222> (337)..(399)  
 <223> Tetanus toxoid P30 epitope

<220>  
 <221> misc\_feature  
 <222> (400)..(564)  
 <223> Murine OPGL, residues 262-316

<400> 13  
 atg aaa cac caa cac caa cat caa cat caa cat caa aaa cct 48  
 Met Lys His Gln His Gln His Gln His Gln His Gln Lys Pro  
 1 5 10 15

09787126-031401

20

gaa gct cag cca ttc gct cat ctg acc atc aac gct gca tcg atc cct 96  
 Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro  
                   20                                  25                                  30

tct ggt tct cat aaa gtt acc ctg tct tct tgg tat cac gac cgc ggt 144  
 Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly  
                   35                                  40                                  45

tgg gct aaa atc tct aac atg acc ctg tct aac ggt aaa ctg aga gtt 192  
 Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val  
                   50                                  55                                  60

aac cag gac ggt ttc tac tac ctg tac gct aac atc tgt ttc aga cat 240  
 Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His  
                   65                                  70                                  75                                  80

cac gaa acc tct ggt tct gtt cca acc gac tac ctg cag ctg atg gtt 288  
 His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val  
   85  90  95

tac gtt gtt aaa acc tct atc aaa atc cca tct tca cat aac ctg atg 336  
 Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met  
   100  105  110

ttc aac aac ttc acc gtt tct ttc tgg ctg agg gta ccg aaa gtt tct 384  
 Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser  
   115  120  125

gct tct cac ctg gaa aac tgg tct ggt aac tct gaa ttc cat ttc tac 432  
 Ala Ser His Leu Glu Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr  
   130  135  140

tct atc aac gtt ggt ggt ttc ttc aaa ctg aga gct ggt gaa gaa atc 480  
 Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile  
                   145                                  150                                  155                                  160

tct atc cag gtt tct aac cct tct ctg ctg gac cca gac cag gac gct 528  
 Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala  
   165  170  175

acc tac ttc ggg gcc ttc aaa gtt cag gac atc gac 564  
 Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp  
   180  185

&lt;210&gt; 14

&lt;211&gt; 188

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

<223> Description of Artificial Sequence: Fusion of  
 murine OPGL, residues 158-316 modified by  
 introduction of tetanus toxoid P30 epitope, and  
 His tag

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&lt;400&gt; 14

Met Lys His Gln His Gln His Gln His Gln His Gln Lys Pro  
 1 5 10 15

Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro  
 20 25 30

Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly  
 35 40 45

Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val  
 50 55 60

Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His  
 65 70 75 80

His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val  
 85 90 95

Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met  
 100 105 110

Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser  
 115 120 125

Ala Ser His Leu Glu Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr  
 130 135 140

Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile  
 145 150 155 160

Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala  
 165 170 175

Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp  
 180 185

&lt;210&gt; 15

&lt;211&gt; 546

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Fusion  
 between murine OPGL, residues 158-316 with tetanus  
 toxoid P2 epitope introduced, and His tag

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(546)

09787126 031401

<220>  
 <221> misc\_binding  
 <222> (1)..(42)  
 <223> His tag

<220>  
 <221> misc\_feature  
 <222> (43)..(336)  
 <223> Murine OPGL, residues 158-255

<220>  
 <221> misc\_feature  
 <222> (382)..(546)  
 <223> Murine OPGL, residues 262-316

<220>  
 <221> misc\_feature  
 <222> (337)..(381)  
 <223> Tetanus toxoid P2 epitope

<400> 15  
 atg aaa cac caa cac caa cat caa cat caa cat caa aaa cct 48  
 Met Lys His Gln His Gln His Gln His Gln His Gln His Gln Lys Pro  
 1 5 10 15

gaa gct cag cca ttc gct cat ctg acc atc aac gct gca tcg atc cct 96  
 Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro  
 20 25 30

tct ggt tct cat aaa gtt acc ctg tct tct tgg tat cac gac cgc ggt 144  
 Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly  
 35 40 45

tgg gct aaa atc tct aac atg acc ctg tct aac ggt aaa ctg aga gtt 192  
 Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val  
 50 55 60

aac cag gac ggt ttc tac tac ctg tac gct aac atc tgt ttc aga cat 240  
 Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His  
 65 70 75 80

cac gaa acc tct ggt tct gtt cca acc gac tac ctg cag ctg atg gtt 288  
 His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val  
 85 90 95

tac gtt gtt aaa acc cct atc aaa atc caa tct tca cat aac ctg atg 336  
 Tyr Val Val Lys Thr Pro Ile Lys Ile Gln Ser Ser His Asn Leu Met  
 100 105 110

cag tac atc aaa gct aat tcg aaa ttc atc ggt atc acc gaa ctg aac 384  
 Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu Asn  
 115 120 125

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23

tgg tct ggt aac tct gaa ttc cat ttc tac tct atc aac gtt ggt ggt 432  
 Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly  
 130 135 140

ttc ttc aaa ctg aga gct ggt gaa gaa atc tct atc cag gtt tct aac 480  
 Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser Ile Gln Val Ser Asn  
 145 150 155 160

cct tct ctg ctg gac cca gac cag gac gct acc tac ttc ggg gcc ttc 528  
 Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe  
 165 170 175

aaa gtt cag gac atc gac 546  
 Lys Val Gln Asp Ile Asp  
 180

&lt;210&gt; 16

&lt;211&gt; 182

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

<223> Description of Artificial Sequence: Fusion  
 between murine OPGL, residues 158-316 with tetanus  
 toxoid P2 epitope introduced, and His tag

&lt;400&gt; 16

Met Lys His Gln His Gln His Gln His Gln His Gln Lys Pro  
 1 5 10 15

Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro  
 20 25 30

Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly  
 35 40 45

Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val  
 50 55 60

Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His  
 65 70 75 80

His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val  
 85 90 95

Tyr Val Val Lys Thr Pro Ile Lys Ile Gln Ser Ser His Asn Leu Met  
 100 105 110

Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu Asn  
 115 120 125

Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly  
 130 135 140

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24

Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser Ile Gln Val Ser Asn  
 145 150 155 160

Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe  
 165 170 175

Lys Val Gln Asp Ile Asp  
 180

&lt;210&gt; 17

&lt;211&gt; 519

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Fusion between  
 murine OPGL, residues 158-316 with tetanus toxoid  
 P2 epitope introduced, and His tag

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(519)

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; (1)..(42)

&lt;223&gt; His tag

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (43)..(432)

&lt;223&gt; Murine OPGL, residues 158-287

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (478)..(519)

&lt;223&gt; Murine OPGL, residues 303-316

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (433)..(477)

&lt;223&gt; Tetanus toxoid P2 epitope

&lt;400&gt; 17

atg aaa cac caa cac caa cat caa cat caa cat caa aaa cct 48  
 Met Lys His Gln His Gln His Gln His Gln His Gln Lys Pro  
 1 5 10 15

gaa gct cag cca ttc gct cat ctg acc atc aac gct gca tcg atc cct 96  
 Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro  
 20 25 30

09787126 031401



25

tct ggt tct cat aaa gtt acc ctg tct tct tgg tat cac gac cgc ggt 144  
 Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly  
           35                          40                          45

tgg gct aaa atc tct aac atg acc ctg tct aac ggt aaa ctg aga gtt 192  
 Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val  
           50                          55                          60

aac cag gac ggt ttc tac tac ctg tac gct aac atc tgt ttc aga cat 240  
 Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His  
           65                          70                          75                          80

cac gaa acc tct ggt tct gtt cca acc gac tac ctg cag ctg atg gtt 288  
 His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val  
                           85                          90                          95

tac gtt gtt aaa acc tct atc aaa atc cca tct tca cat aac ctg atg 336  
 Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met  
                           100                          105                          110

aaa ggt ggt tct acc aaa aac tgg tct ggt aac tct gaa ttc cat ttc 384  
 Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe  
           115                          120                          125

tac tct atc aac gtt ggt ggt ttc ttc aaa ctg aga gct ggt gaa gaa 432  
 Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu  
           130                          135                          140

cag tac atc aaa gct aat tgc aaa ttc atc ggt atc acc gaa ctg gac 480  
 Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu Asp  
           145                          150                          155                          160

gct acc tac ttc ggg gcc ttc aaa gtt cag gac atc gac 519  
 Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp  
                           165                          170

&lt;210&gt; 18

&lt;211&gt; 173

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

<223> Description of Artificial Sequence: Fusion between  
 murine OPGL, residues 158-316 with tetanus toxoid  
 P2 epitope introduced, and His tag

&lt;400&gt; 18

Met Lys His Gln His Gln His Gln His Gln His Gln Lys Pro  
   1                          5                          10                          15

Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro  
           20                          25                          30

Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly

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35 40 45

Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val  
50 55 60

Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His  
65 70 75 80

His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val  
85 90 95

Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met  
100 105 110

Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe  
115 120 125

Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu  
130 135 140

Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu Asp  
145 150 155 160

Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp  
165 170

&lt;210&gt; 19

&lt;211&gt; 519

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Fusion between  
murine OPGL, residues 158-316 with tetanus toxoid  
P30 epitope introduced, and His tag

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(519)

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; (1)..(42)

&lt;223&gt; His tag

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (43)..(231)

&lt;223&gt; Murine OPGL, residues 158-220

&lt;220&gt;

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del  
910  
Cont

<221> misc\_feature  
 <222> (295)..(519)  
 <223> Murine OPGL, residues 242-316

<220>  
 <221> misc\_feature  
 <222> (232)..(294)  
 <223> Tetanus toxoid P30 epitope

<400> 19  
 atg aaa cac caa cac caa cat caa cat caa cat caa cat caa aaa cct 48  
 Met Lys His Gln His Gln His Gln His Gln His Gln His Gln Lys Pro  
 1 5 10 15  
 gaa gct cag cca ttc gct cat ctg acc atc aac gct gca tcg atc cct 96  
 Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro  
 20 25 30  
 tct ggt tct cat aaa gtt acc ctg tct tct tgg tat cac gac cgc ggt 144  
 Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly  
 35 40 45  
 tgg gct aaa atc tct aac atg acc ctg tct aac ggt aaa ctg aga gtt 192  
 Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val  
 50 55 60  
 aac cag gac ggt ttc tac tac ctg tac gct aac atc tgt ttc aac aac 240  
 Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Asn Asn  
 65 70 75 80  
 ttc acc gtt tct ttc tgg ctg agg gta ccg aaa gtt tct gct tct cac 288  
 Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser Ala Ser His  
 85 90 95  
 ctg gaa gtt aaa acc tct atc aaa atc cca tct tca cat aac ctg atg 336  
 Leu Glu Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met  
 100 105 110  
 aaa ggt ggt tct acc aaa aac tgg tct ggt aac tct gaa ttc cat ttc 384  
 Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe  
 115 120 125  
 tac tct atc aac gtt ggt ggt ttc ttc aaa ctg aga gct ggt gaa gaa 432  
 Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu  
 130 135 140  
 atc tct atc cag gtt tct aac cct tct ctg ctg gac cca gac cag gac 480  
 Ile Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp  
 145 150 155 160  
 gct acc tac ttc ggg gcc ttc aaa gtt cag gac atc gac 519  
 Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp  
 165 170

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*Sub  
 A10  
 cont*

&lt;210&gt; 20

&lt;211&gt; 173

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

<223> Description of Artificial Sequence: Fusion between  
murine OPGL, residues 158-316 with tetanus toxoid  
P30 epitope introduced, and His tag

&lt;400&gt; 20

Met Lys His Gln His Gln His Gln His Gln His Gln His Gln Lys Pro  
1 5 10 15

Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro  
20 25 30

Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly  
35 40 45

Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val  
50 55 60

Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Asn Asn  
65 70 75 80

Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser Ala Ser His  
85 90 95

Leu Glu Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met  
100 105 110

Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe  
115 120 125

Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu  
130 135 140

Ile Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp  
145 150 155 160

Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp  
165 170

&lt;210&gt; 21

&lt;211&gt; 68

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic PCR  
primer

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 104150 92128760

Sub  
a10  
Cont

<400> 21  
agctgcagggt agtcggttgg aacagaacca gaggtttcgt gatgtctgaa acagatgtta 60  
gcgtacag 68

<210> 22  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic PCR  
primer

<400> 22  
ctcatctgac catcaacgct gcat 24

<210> 23  
<211> 64  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic PCR  
primer

<400> 23  
tttcggtacc ctccagccaga aagaaacggt gaagttgttg aaacagatgt tagcgtacag 60  
gtag 64

<210> 24  
<211> 61  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic PCR  
primer

<400> 24  
tgagggtacc gaaagtttct gcttctcacc tggaagttaa aaccctatc aaaatccaat 60  
c 61

<210> 25  
<211> 63  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic PCR

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Sub  
a/o  
cont

primer

<400> 25  
tttcggtacc ctcagccaga aagaaacggt gaagttgttg aacatcaggt tatgtgaaga 60  
ttg 63

<210> 26  
<211> 62  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic PCR  
primer

<400> 26  
tgagggtacc gaaagtttct gcttctcacc tggaaaactg gtctggtaac tctgaattcc 60  
at 62

<210> 27  
<211> 79  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic PCR  
primer

<400> 27  
tacctgcagc tgatggttta cgttgttaaa acccctatca aaatccaatc ttcacataac 60  
ctgatgcagt acatcaaag 79

<210> 28  
<211> 83  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic PCR  
primer

<400> 28  
tggaattcag agttaccaga ccagttcagt tcggtgatac cgatgaattt cgaattagct 60  
ttgatgtact gcatcagggt atg 83

<210> 29  
<211> 49  
<212> DNA  
<213> Artificial Sequence

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Sub  
A10  
Cont

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Synthetic PCR primer

&lt;400&gt; 29

gaatttcgaa ttagctttga tgtactgttc ttcaccagct ctcagtttg

49

&lt;210&gt; 30

&lt;211&gt; 53

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Synthetic PCR primer

&lt;400&gt; 30

gctaattcga aattcatcgg taccaccgaa ctggacgcta cctacttcgg ggc

53

&lt;210&gt; 31

&lt;211&gt; 26

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Synthetic PCR primer

&lt;400&gt; 31

cttactagtc gatgtcctga actttg

26

&lt;210&gt; 32

&lt;211&gt; 74

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Synthetic PCR primer

&lt;400&gt; 32

agtggaaattc agagttacca gaccagtttt tggtagaacc acctttcatc aggttatgtg 60  
aagatgggat ttg 74

&lt;210&gt; 33

&lt;211&gt; 65

&lt;212&gt; DNA

&lt;213&gt; Clostridium tetani

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Sul  
a10  
cont

<210> 34  
<211> 15  
<212> PRT  
<213> Clostridium tetani

<400> 34  
Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu  
1 5 10 15

```
<210> 35
<211> 21
<212> PRT
<213> Clostridium tetani
```

<400> 35  
Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser  
1 5 10 15

Ala Ser His Leu Glu  
20

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